

1. **ВВЕДЕНИЕ**  
 2. **ОБЪЕКТ И ПРЕДМЕТ ИССЛЕДОВАНИЯ**  
 3. **ЦЕЛИ И ЗАДАЧИ ИССЛЕДОВАНИЯ**  
 4. **МЕТОДЫ ИССЛЕДОВАНИЯ**  
 5. **РЕЗУЛЬТАТЫ ИССЛЕДОВАНИЯ**  
 6. **ВЫВОДЫ**  
 7. **СПИСОК ЛИТЕРАТУРЫ**  
 8. **ПРИЛОЖЕНИЯ**  
 9. **УКАЗАТЕЛЬ**  
 10. **СЛОВАРЬ**  
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 207. **УКАЗАТЕЛЬ**  
 208. **СЛОВАРЬ**  
 209.

(1) ~~GENERAL~~ INFORMATION:

(i) APPLICANT: HOGREFE, Holly  
HANSEN, Connie J

(ii) **TITLE OF INVENTION:** Polymerase Enhancing Factor (PEF) Extracts, PEF Protein Complexes, Isolated PEF Proteins, and Methods for Purifying and Identifying Them

(iii) NUMBER OF SEQUENCES: 89

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: David J. Kulik, Evenson, McKeown, Edwards & Lenahan P.L.L.C.

(B) STREET: 1200 G Street, NW Suite 700

(C) CITY: Washington

(D) STATE: DC

(F) ZIP: 20005

(v) **COMPUTER READABLE FORM:**

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE: 24-OCT-1997

(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: KULIK, David J

(B) REGISTRATION NUMBER: 36,576

(C) REFERENCE/DOCKET NUMBER: 1486/43163cp

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 202 628-8800

(B) TELEFAX: 202 628-8844

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Xaa Xaa Leu His His Val Lys Leu Ile Tyr Ala Thr Xaa Xaa Xaa  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Xaa Xaa Xaa Pro Asp Trp Xaa Xaa Arg Xaa Glu Xaa Leu Xaa Xaa  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Xaa Tyr Asp Ala Val Ile Met Ala Ala Ala Val Val Asp Phe Arg Pro  
1 5 10 15

Lys

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ala Asp Leu Val Val Gly Asn Thr Leu Glu Ala Phe Gly Ser Glu Glu  
1 5 10 15

Asn Gln Val Val Leu Ile Gly Arg  
20

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gly Ala Met Leu His His Val Lys Leu Ile Tyr Ala Xaa Lys Leu Arg  
1 5 10 15

Lys

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Gly Ala Met Leu His His Val Lys Leu Ile Tyr Ala Thr Lys Xaa Xaa  
1                      5                      10                      15

Arg Lys

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Leu His His Val Lys Leu Ile Tyr Ala Thr Lys Leu  
1                      5                      10

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gly	Xaa	Xaa	Xaa	Pro	Asp	Trp	Xaa	Xaa	Lys	Phe	Arg	Lys	Glu	Glu	Ser
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Gly	Ala	Ile	Leu	Leu	Pro	Asp	Trp	Lys	Ile	Arg	Lys	Glu	Ile	Leu	Ile
1				5					10					15	

Glu

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Xaa	Met	His	His	Val	Ile	Lys	Leu	Xaa	Tyr	Ala	Thr	Xaa	Ser	Arg	Lys
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Leu	Tyr	Leu	Val	Arg	Pro	Asp	Trp	Lys	Arg	Arg	Lys	Glu	Ile	Leu
1				5					10					15	

Ile Glu

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CAYCAYGAHA ARYTHATTTA CGC

23

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs

[illegible]

(iv) ANTI-SENSE: YES

GCCATDATNA CDGCRTCGTA TTT

23

(D) TOPOLOGY: unknown

(iv) ANTI-SENSE: NO

CAYCAYGAHA ARYTHATATA CGC

23

(D) TOPOLOGY: unknown

(iv) ANTI-SENSE: YES

ARDACDACYT GRTTTTCTTC

20



(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1209 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATGCTTCACC	ACGTCAAGCT	AATCTACGCC	ACAAAAAGTC	GAAAGCTAGT	TGGAAAAAAG	60
ATAGTCNNNN	NNNNNCCAGG	GAGTATTGCG	GCTTTGGATG	TGAAAGCTTG	TGAGGGACTA	120
ATTAGGCATG	GGGCCGAAGT	TCATGCAGTG	ATGAGTGAGG	CAGCCACCAA	GATAATTCAT	180
CCTTATGCAT	GGAATTTGCC	CACGGGAAAT	CCAGTCATAA	CTGAGATCAC	TGGATTTATC	240
GAGCATGTTG	AGTTAGCAGG	GGAACATGAG	AATAAAGCAG	ATTTAATTTT	GGTTTGTCTT	300
GCCACTGCCA	ACACAATTAG	TAAGATTGCA	TGTGGAATAG	ATGATACTCC	AGTAACTACA	360
GTCGTGACCA	CAGCATTTC	CCACATTCCA	ATTATGATAG	CCCCAGCAAT	GCATGAGACA	420
ATGTACAGGC	ATCCCATAGT	AAGGGAGAAC	ATTGAAAGGT	TAAAGAAGCT	TGGCGTTGAG	480
TTTATAGGAC	CAAGAATTGA	GGAGGGAAAG	GCAAAAGTTG	CAAGCATTGA	TGAAATAGTT	540
TACAGAGTTA	TTAAAAAGCT	CCACAAAAAA	ACATTGGAAG	GGAAGAGAGT	CCTAGTAACG	600
GCGGGAGCAA	CAAGAGAGTA	CATAGATCCA	ATAAGATTCA	TAACAAATGC	CAGCAGTGGA	660
AAAATGGGAG	TAGCGTTGGC	TGAAGAAGCA	GATTTTAGAG	GAGCTGTTAC	CCTCATAAGA	720
ACAAAGGGAA	GTGTAAAGGC	TTTLAGAATC	AGAAAAATCA	AATTGAAGGT	TGAGACAGTG	780
GAAGAAATGC	TTTCAGCGAT	TGAAAATGAG	TTGAGGAGTA	AAAAGTATGA	CGTAGTTATT	840
ATGGCAGCTG	CTGTAAGCGA	TTTLAGGCCA	AAAATTAAAG	CAGAGGGAAA	AATTAAAAGC	900
GGAAGATCAA	TAACGATAGA	GCTCGTTCCN	NNNAATCCCA	AAATCATTGA	TAGAATAAAG	960
GAAATTCAAC	CAAATGTCTT	TCTTGTGGA	TTTAAAGCAG	AACTTCAAAA	AGAAAAGCTT	1020
ATAGAAGAAG	GTAAAAGGCA	GATTGAGAGG	GCCAAGGCTG	ACTTAGTCGT	TGGTAACACA	1080
TTGGAAGCCT	TTGGAAGCGA	GGAAAACCAA	GTAGTATTAA	TTGGCAGAGA	TTTCACAAAA	1140



205

**Xaa Leu Ser**

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CATAGCGAAT TCGCAAAACC TTTCGCGGTA TGG

33

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ACTACGGAAT TCCACGGAAA ATGCCGCTCA TCC

33

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GGCGTTTCCG TTCTTCTTCG

20

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CCATCTCACG CGCCAGTTTC

20

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GAGGAGAGCA GGAAAGGTGG AAC

23

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GCTGGGAGAA GACTTCACTG G

21

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GAGCTTGCTC AACTTTATC

19

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GATAGAGATA GTTCTGGAG ACG

23

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CGGGATATCG ACATTCTGC ACC

23

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

[illegible]

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

GAGTTAAATG CCTACACTGT ATCT

24

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

CAGGACTCAG AAGCTGCTAT CGAA

24

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

CTGCACGTGC CCTGTAGGAT TTGT

24

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CCAGAYTGGA ARWKNAGGAA AGA

23

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CCAGAYTGGA ARWKNAGAAA AGA

23

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CCAGAYTGGA ARWKNAGGAA GGA

23

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CCAGAYTGGA ARWKNAGAAA GGA

23

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CAGAGTGGGC AGAGAGGCTN TTGTTAAGGG GAAATTAATC GACGTGGAAA  
AGGAAGGAAA 60

AGTCGNTATT CCTCCAAGGG AATA

84

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

[illegible]

(v) FRAGMENT TYPE: internal

Glu Trp Ala Glu Arg Leu Leu Leu Arg Gly Asn Xaa Ser Lys Trp Lys  
1 5 10 15

Arg Lys Glu Lys Ser Xaa Phe Leu Gln Gly Asn  
20 25

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: unknown

(iii) HYPOTHETICAL: YES

(v) FRAGMENT TYPE: internal

Arg Val Gly Arg Glu Ala Xaa Val Lys Gly Lys Leu Ile Glu Val Glu  
1 5 10 15

Lys Glu Gly Lys Val Xaa Ile Pro Pro Arg Glu  
20 25

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: unknown

(iii) HYPOTHETICAL: YES

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Gln Ser Gly Gln Arg Gly Xaa Cys Xaa Gly Glu Ile Asn Arg Ser Gly  
1 5 10 15

Lys Gly Arg Lys Ser Arg Tyr Ser Ser Lys Gly Leu  
20 25

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 129 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CTGCCCACTC TGAGGTCATA ACCTGCTGGT TGGAGCCATT CTCAGAAAA TGGCTCTATA 60  
AGTATTTCTT TTCTGATTTT CCAGTCTGGA AGTAGCATTT TACCACCGAA ACCTTTATTT 120  
TTAATTTAA 129

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Xaa Ile Lys Asn Lys Gly Phe Gly Gly Lys Met Leu Leu Pro Asp Trp  
1 5 10 15

Lys Ile Arg Lys Glu Ile Leu Ile Glu Pro Phe Ser Glu Glu Trp Leu  
 20 25 30

Gln Pro Ala Gly Tyr Asp Leu Arg Val Gly  
 35 40

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 740 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

TCCTCCAAGG GAATACGCCT TAATCCTAAC CCTCGAGAGG ATAAAGTTGC CCGACGATGT	60
TATGGGGGAT ATGAAGATAA GGAGCAGTTT AGCAAGAGAA GGGGTTATTG GTTCTTTTGC	120
TTGGGTTGAC CCAGGATGGG ATGGAAACTT AACACTAATG CTCTACAATG CCTCAAATGA	180
ACCTGTGCGAA TTAAGATATG GAGAGAGATT TGTGCAGATC GCATTTATAA GGCTAGAGGG	240
TCCGGCAAGA AACCCCTTACA GAGGAACTA TCAGGGGAGC ACAAGGTTAG CGTTTTCAAA	300
GAGAAAGAAA CTCTAGCGTC TTTTCAATAG CATCCTCAAT ATCTCGTGTG AAGTAATCAA	360
TGTAAATACT TGCTGGGTGG GTTTTTAGGG ATTCAAATC GTAAGATGGG CCTGTATAGC	420
AGAAAACTAT TTTTGCCTCT TCTTCATTTA TCTTTCTGTG AATAAAAAAT CCAACATCCA	480
CACTAGTTCC AAAAGATATT GTTTGCGTGA TTACCAACAA GATCTTGGCA TTATTTTTGA	540
TCTTATACTC TATTCTCCTT TCTCCCTCCA ATTTGCCCAA AATAAACCTG GGTAGTATAC	600
ATCACTCCT CTCTTTTAAA TTCCTATAAA TTCGTACATA GTTTAGAAAA ATGTCAAATT	660
CTTNTTCCC TGTTAAATTA ACCNCNAAAT CTTTATNANN AANCTTTTTA TAATTCCCAA	720
AACCCCTAAT TTTCCCCTTN	740

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown



Lys Leu Thr Xaa Lys Ser Leu Xaa Xaa Xaa Phe Leu Xaa Phe Pro Lys  
 225 230 235 240

Pro Leu Ile Phe Pro Xaa  
 245

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Pro Pro Arg Glu Tyr Ala Leu Ile Leu Thr Leu Glu Arg Ile Lys Leu  
 1 5 10 15

Pro Asn Asn Val Met Gly Asp Met Lys Ile Arg Ser Ser Leu Ala Arg  
 20 25 30

Glu Gly Val Ile Gly Ser Phe Ala Trp Val Asp Pro Gly Trp Asp Gly  
 35 40 45

Asn Leu Thr Leu Met Leu Tyr Asn Ala Ser Asn Glu Pro Val Glu Leu  
 50 55 60

Arg Tyr Gly Glu Arg Phe Val Gln Ile Ala Phe Ile Arg Leu Glu Gly  
 65 70 75 80

Pro Ala Arg Asn Pro Tyr Arg Gly Asn Tyr Gln Gly Ser Thr Arg Leu  
 85 90 95

Ala Phe Ser Lys Arg Lys Lys Leu Xaa Arg Leu Phe Asn Ser Ile Leu  
 100 105 110

Asn Ile Ser Cys Glu Val Ile Asn Val Asn Thr Cys Trp Val Gly Phe  
 115 120 125

Xaa Gly Phe Lys Leu Val Arg Trp Ala Cys Ile Ala Glu Asn Tyr Phe  
 130 135 140

Cys Leu Phe Phe Ile Tyr Leu Ser Val Asn Lys Lys Ser Asn Ile His  
 145 150 155 160

Thr Ser Ser Lys Arg Tyr Cys Leu Arg Asp Tyr Gln Gln Asp Leu Gly  
 165 170 175

Ile Ile Phe Asp Leu Ile Leu Tyr Ser Pro Phe Ser Leu Gln Phe Ala  
 180 185 190

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His Xaa Phe Gln Lys Ile Leu Phe Ala Xaa Leu Pro Thr Arg Ser Trp  
                   165                                  170                                  175  
 His Tyr Phe Xaa Ser Tyr Thr Leu Phe Ser Phe Leu Pro Pro Ile Cys  
                   180                                  185                                  190  
 Pro Lys Xaa Thr Trp Val Val Tyr Ile His Ser Ser Leu Leu Asn Ser  
                   195                                  200                                  205  
 Tyr Lys Phe Val His Ser Leu Glu Lys Cys Gln Ile Leu Xaa Ser Leu  
                   210                                  215                                  220  
 Leu Asn Xaa Pro Xaa Asn Leu Tyr Xaa Xaa Xaa Phe Tyr Asn Ser Gln  
                   225                                  230                                  235                                  240  
 Asn Pro Xaa Phe Ser Pro  
                                   245

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Met Leu His His Val Lys Leu Ile Tyr Ala Thr Lys Ser Arg Lys Leu  
 1                  5                                  10                                  15  
 Val Gly Lys Lys Ile Val Xaa Xaa Xaa Pro Gly Ser Ile Ala Ala  
                   20                                  25                                  30

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CTATTGAGTA CGAACGCCAT C

21

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GTCACGCTTG CTCCACTCCG

20

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Methanococcus Jannaschii

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Met Ile Ser Glu Ile Met His Pro Thr Lys Leu Leu Lys Gly Thr Lys  
1                      5                      10                      15

Ser Lys Leu Leu Glu Asn Lys Lys Ile Leu Val Ala Val Thr Ser Ser  
                    20                      25                      30

Ile Ala Ala Ile Glu Thr Pro Lys Leu Met Arg Glu Leu Ile Arg His  
                    35                      40                      45

Gly Ala Glu Val Tyr Cys Ile Ile Thr Glu Glu Thr Lys Lys Ile Ile  
50                      55                      60

Gly Lys Glu Ala Leu Lys Phe Gly Cys Gly Asn Glu Val Tyr Glu Glu



Ala Lys Glu Arg Leu Asn Lys Tyr Asn Leu Asn Met Ile Ile Ala Asn  
 370 375 380

Asp Leu Ser Lys Xaa Xaa His Tyr Phe Gly Asp Asp Tyr Ile Glu Val  
 385 390 395 400

Tyr Ile Ile Thr Lys Tyr Glu Val Glu Lys Ile Ser Gly Ser Lys Lys  
 405 410 415

Xaa Glu Ile Ser Glu Arg Ile Val Glu Lys Val Lys Lys Leu Val Lys  
 420 425 430

Ser Xaa Xaa Xaa Xaa  
 435

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Escherichia coli

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Met Lys Ala Arg Gln Gln Lys Tyr Cys Asp Lys Ile Ala Asn Phe Trp  
 1 5 10 15

Cys His Pro Thr Gly Lys Ile Ile Met Ser Leu Ala Gly Lys Lys Ile  
 20 25 30

Val Leu Gly Val Ser Gly Gly Ile Ala Ala Tyr Lys Thr Pro Glu Leu  
 35 40 45

Val Arg Arg Leu Arg Asp Arg Gly Ala Asp Val Arg Val Ala Met Thr  
 50 55 60

Glu Ala Ala Lys Ala Phe Ile Thr Pro Leu Ser Leu Gln Ala Val Ser  
 65 70 75 80

Gly Tyr Pro Val Ser Asp Ser Leu Leu Asp Pro Ala Ala Glu Ala Ala  
 85 90 95

Met Gly His Ile Glu Leu Gly Xaa Xaa Xaa Xaa Lys Trp Ala Asp Leu  
 100 105 110

Val Ile Leu Ala Pro Ala Thr Ala Asp Leu Ile Ala Arg Val Ala Ala

125

Asn	Ser	Asp	Asn	Asn	Ala	Leu	His	Leu	Phe	Trp	Gln	Asp	Gly	Asp	Lys
				405					410					415	

[illegible]

Val Leu Pro Leu Glu Arg Lys Glu Leu Leu Gly Gln Leu Leu Leu Asp  
420 425 430

Glu Ile Val Thr Arg Tyr Asp Glu Lys Asn Arg Arg  
435 440

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Xaa Gly Xaa Xaa Asp Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa  
1 5 10

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Phe Ala Trp Val Asp Pro Gly Trp Asp Gly Asn Thr Leu Met  
1 5 10

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: unknown



(v) FRAGMENT TYPE: internal

Ala Gly Trp Ile Asp Ala Gly Phe Lys Gly Lys Ile Thr Leu  
1 5 10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ser Ala Val His Asp Pro Gly Tyr Glu Gly Arg Pro Glu Tyr  
1 5 10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Pro Thr Ile Val Asp Ala Gly Phe Glu Gly Gln Leu Thr Ile  
1 5 10

(2) INFORMATION FOR SEQ ID NO:58:

	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405	2406	2407	2408	2409	2410	2411	2412	2413	2414	2415	2416	2417	2418	2419	2420	2421	2422	2
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- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 14 amino acids  
    (B) TYPE: amino acid  
    (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Ala His Arg Ile Asp Pro Gly Trp Ser Gly Cys Ile Val Leu  
1                    5                    10

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 24 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GAGTTAAATG CCTACACTGT ATCT

24

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 24 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:



## (2) INFORMATION FOR SEQ ID NO:61:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CTGCACGTGC CCTGTAGGAT TTGT

24

## (2) INFORMATION FOR SEQ ID NO:62:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CTATTGAGTA CGAACGCCAT C

21

## (2) INFORMATION FOR SEQ ID NO:63:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GTCACGCTTG CTCCACTCCG

20

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GAGGAGAGCA GGAAAGGTGG AAC

23

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GCTGGGAGAA GACTTCACTG G

21

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

His His Val Lys Leu Ile Tyr Ala  
1 5

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Lys Tyr Asp Ala Val Ile Met Ala  
1 5

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Glu Glu Asn Gln Val Val Leu  
1 5

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Pro Asp Trp Lys Ile Arg Lys Glu  
1 5

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 471 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

ATGCTACTTC CAGACTGGAA AATCAGAAAA GAAATACTTA TAGAGCCATT TTCTGAAGAA	60
TCGCTCCAAC CAGCAGGTTA TGACCTCAGA GTGGGCAGAG AGGCTTTTGT TAAGGGGAAA	120
TTAATCGACG TGGAAAAGGA AGGAAAAGTC GTTATTCCTC CAAGGGAATA CGCCTTAATC	180
CTAACCCCTCG AGAGGATAAA GTTGCCCGAC GATGTTATGG GGGATATGAA GATAAGGAGC	240
AGTTTAGCAA GAGAAGGGGT TATTGGTTCT TTTGCTTGGG TTGACCCAGG ATGGGATGGA	300
AACTTAACAC TAATGCTCTA CAATGCCTCA AATGAACCTG TCGAATTAAG ATATGGAGAG	360
AGATTTGTGC AGATCGCATT TATAAGGCTA GAGGGTCCGG CAAGAAACCC TTACAGAGGA	420
AACTATCAGG GGAGCACAAG GTTAGCGTTT TCAAAGAGAA AGAAACTCTA G	471

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 156 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Met Leu Leu Pro Asp Trp Lys Ile Arg Lys Glu Ile Leu Ile Glu Pro  
1 5 10 15  
Phe Ser Glu Glu Ser Leu Gln Pro Ala Gly Tyr Asp Leu Arg Val Gly  
20 25 30  
Arg Glu Ala Phe Val Lys Gly Lys Leu Ile Asp Val Glu Lys Glu Gly  
35 40 45  
Lys Val Val Ile Pro Pro Arg Glu Tyr Ala Leu Ile Leu Thr Leu Glu  
50 55 60  
Arg Ile Lys Leu Pro Asp Asp Val Met Gly Asp Met Lys Ile Arg Ser  
65 70 75 80  
Ser Leu Ala Arg Glu Gly Val Ile Gly Ser Phe Ala Trp Val Asp Pro  
85 90 95  
Gly Trp Asp Gly Asn Leu Thr Leu Met Leu Tyr Asn Ala Ser Asn Glu  
100 105 110  
Pro Val Glu Leu Arg Tyr Gly Glu Arg Phe Val Gln Ile Ala Phe Ile  
115 120 125  
Arg Leu Glu Gly Pro Ala Arg Asn Pro Tyr Arg Gly Asn Tyr Gln Gly  
130 135 140  
Ser Thr Arg Leu Ala Phe Ser Lys Arg Lys Lys Leu  
145 150 155

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:





(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Val	Gly	Leu	Ile	Asp	Ser	Asp	Tyr	Gln	Gly	Gln	Leu	Met	Ile
1				5					10				

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Ala	Gly	Val	Val	Asp	Arg	Asp	Tyr	Thr	Gly	Glu	Val	Lys	Val
1				5					10				

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO



(iv) ANTI-SENSE: NO.

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Ala Gly Val Ile Asp Glu Asp Tyr Arg Gly Asn Val Gly Val  
1                      5                      10

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Thr Gly Leu Ile Asp Pro Gly Phe Gln Gly Glu Leu Lys Leu  
1                      5                      10

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GACGACGACA AGATGCTACT TCCAGACTGG AAA

33

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GGAACAAGAC CCGTCCCACT TTCACAGATG AAGAG

35

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

GAGGAGAGCA GGAAAGGTGG AAC

23

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

CTCCATGTCC CAACTCCGAT CAC

23

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

GGTTTCCCA GTCACGACGT TGTAACACGA CGGCCAGT

38

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GGUUUCCCA GUCACGACGU UGUAAAACGA CGGCCAGU

38

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GACGACGACA AGATGCCCTG CTCTGAAGAG ACACC

35

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GGAACAAGAC CCGTTTAATT CTTTCAGTG GAACC

35

CGTTTCAGTGGAACC